

Db 103 SKGRKEMNQVEISPTVYRDVTGCGRKKQYRFYWSSETLFDGNCNGLNGTIVQISCKEQ 162
 QY 123 NVVCTCHAGFFLRNFCVSCNCKKS 148
 Db 163 NTICTCHAGFFLRNFCVSCNCKKN 188

RESULT 2

Q95185 ID Q95185 PRELIMINARY; PRT; 189 AA.
 AC Q95185
 DT 01-FEB-1997 (Tremblrel. 02, Created)
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
 GN TNFR_1
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia, Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN 111
 RP SEQUENCE FROM N.A.
 RA Duthie S., Nasir L., Ekersall P.D.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: 072344; AAB95089.1;
 DR HSSP: P19438; 1RX1.
 DR InterPro: IPR000561; FGF-like.
 DR Pfam: PF00020; TNFR_C6; 3.
 DR ProDom: PD000771; TNFR_C6; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS01186; FGF_2; UNKNOWN_1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS00050; TNFR_NGFR_2; 3.
 FT NON_TER 189 189
 SQ SEQUENCE 189 AA: 21420 MW: 717680 P804070E6 CRC64;

Query Match 77.7%; Score 731; DB 6; Length 189;
 Best Local Similarity 85.5%; Pred. No. 1.7e 68;
 Matches 124; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
 QY 4 CPQGYIHPQNNISLCTKCHKYTYLYNCPGPGQDTDRPEESGFTASENHILRHCLSCS 63
 Db 44 CPQGYIHPQNNISLCTKCHKYTYLYNCPGPGQDTDRPEESGFTASENHILRHCLSCS 103
 QY 64 KPEKMGCGVEISS'TVLRGDTW'G'PKNYRHYWSENLFQ'FN'SL'LN'FVHLSC'PKQN 123
 Db 104 KGRKEMVQVEISPTVYRGTW'G'PKNYRHYWSENLFQ'FN'SL'LN'FVHLSC'PKQN 163
 QY 124 IVCTCHAGFFLRNFCVSCNCKKS 148
 Db 164 TVCTCHAGFFLRNFCVSCNCKKN 188

RESULT 3

Q99MM1 ID Q99MM1 PRELIMINARY; PRT; 413 AA.
 AC Q99MM1
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE WSL-1-LIKE PROTEIN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN 111
 RP SEQUENCE FROM N.A.
 RA STRAIN-129/SV;
 RX MEDLINE-21158384; PubMed 11261933;
 RA Wang E.C.Y., Kittson J.L., Thirn A., Williams J.L., Farrow S.N.,

RA Owen M.J.;
 RT "Genomic structure, expression, and chromosome mapping of the mouse
 RT homologue for the WSL-1 (DR3, Apo3, TRAMP, IAPD, IR3, TNFRSF12)
 RT gene.";
 RL Immunogenetics 53:59-63(2001).
 DR EMBL: AF329969; AAK11256.1;
 SQ SEQUENCE 413 AA: 44453 MW: 69F21B85D0DABAF CRC64;

Query Match 21.5%; Score 202; DB 11; Length 413;
 Best Local Similarity 31.4%; Pred. No. 2.6e-13;
 Matches 48; Conservative 19; Mismatches 58; Indels 28; Gaps 7;
 QY 18 CTCTKCHKYTYLYNCPGPGQDTDRPEESGFTASENHILRHCLSCSKCKEMCGVEISS 76
 Db 54 CCGCGCKCHKYWKAPTAPEQCNSTCLPGYSDFF:FNHFKTHCTRCQVCDREALQVLEN 113
 QY 77 CTVDRTVWGCKKNYRHYWSENLFQ'FN'SL'LN'FVHLSC'-----QEKONTVCT 127
 Db 114 CSAKSDIHGG'QSG'-----W'-----CVKSTVCGKSSFSVPGKATFEVHEATPPR 162
 QY 128 CHAGFFLRNFCVSC-----SNCKKSLPCTKIC 155
 Db 163 CLP:PYIRGNDCTSCPTGFSVCPKA--CTAVC 193

RESULT 4

Q9ER63 ID Q9ER63 PRELIMINARY; PRT; 147 AA.
 AC Q9ER63
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-JUN-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR P60 HOMOLOGUE 1.
 GN TNFRSF1A1 OR TNFRH1
 OS Mus musculus domesticus (western European house mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10092;
 RN 111
 RP SEQUENCE FROM N.A.
 RA STRAIN-129 SV;
 RX MEDLINE-20519229; PubMed 11063728;
 RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
 RA Lane N., Reik W., Walter J.;
 RT "Sequence and functional comparison in the Beckwith-Wiedemann region:
 RT implications for a novel imprinting centre and extended imprinting.";
 RL Hum. Mol. Genet. 9:2691-2706(2000)
 RN 121
 RP SEQUENCE FROM N.A.
 RC STRAIN-129 SV;
 RA Engemann S.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A1278264; CAC16405.1;
 DR EMBL: A1278505; CAC27352.1;
 DR MGD: MGI:1930269; Tnfrsf1a1.
 DR InterPro: IPR000345; Cyt_c_heme_bind.
 DR InterPro: IPR001368; TNFR_C6; 3.
 DR Pfam: PF00020; TNFR_C6; 3.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00140; CYT_C_HEME_C; UNKNOWN_1.
 DR PROSITE: PS00050; TNFR_NGFR_2; 2.
 KW Receptor.
 SQ SEQUENCE 147 AA: 16253 MW: 7644271445170C9 CRC64;

Query Match 21.4%; Score 200.5; DB 11; Length 147;
 Best Local Similarity 33.6%; Pred. No. 1.6e-13;
 Matches 42; Conservative 16; Mismatches 69; Indels 7; Gaps 4;
 QY 4 CPQGYIHPQNNISLCTKCHKYTYLYNCPGPGQDTDRPEESGFTASENHILRHCLSCS 63
 Db 44 CPQGYIHPQNNISLCTKCHKYTYLYNCPGPGQDTDRPEESGFTASENHILRHCLSCS 103


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Query Match      21.3%; Score 200.5; DB 4; Length 418;
Best Local Similarity 29.8%; Pred. No. 3-7e-13;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps

QY    11 HPCNNSTGICKCHAGCTVYNHCPQGDHDKCKFCSSGF IASENHKK-HCISCSKCKRKM 69
DB    11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY    40 HKKGIGFGRCPACHIKAKATEPKGNLSLTLWTDITFLAWNIHNS-SFAKQAITEGA 99
DB    40 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY    70 GOVEISSIVDPTGVATPEKNQYEDHWSENLEP-----FN'SL'LN-GTVH----LSQG 119
DB    70 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY    100 SOVALENCASAVDRCCCKIQWEVEG---CVSCVSSSHFYCGQCUGAUKHKHTKLICS 156
DB    100 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY    120 EKQNTVCTHAGFLRENECVSC--SNCKKSLECTKLC 155
DB    120 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY    157 RDTTCGTCLDPFYEHGGVVSQPTSTLTGSGPR--PCAAYC 195
DB    157 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
Q9ER62 PRELIMINARY; PRT: 141 AA.
ID Q9ER62 AC Q9ER62
DC 01-MAP-2001 (TRIMBirel_16, Created)
DT 01-JUN-2001 (TRIMBirel_16, last sequence update)
DI 01-JUN-2001 (TRIMBirel_17, last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR p60 HOMOLOGUE 2
DS TNFRSF12 OR TNFR12.
GS Mus musculus domesticus (western European house mouse).
OC Pakayota, Metazoa, Chordata, Glires, Velebrata; Eutelestomi,
OC Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
OX NCBI TaxID=10092; [1]
RN 1 J EXP MED 199;
RP SEQUENCE FROM N.A.
RC STRAIN=129 SV;
RX MEDLINE=20514229; PubMed=11063728;
RA Engemann S., Strodick M., Paulsen M., Franck O., Reinhardt K.,
RA Lane N., Reik W., Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region:
RT implications for a novel imprinting centre and extended imprinting." ;
RL Hum. Mol. Genet. 9:2601-2704(2000)
RN 12 J
RP SEQUENCE FROM N.A.
RC STRAIN=129 SV;
RX Engemann S.;
RA Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DL EMRI: A127A265; CAC16406.1;
DR EMRI: AJ276505; CAC27353.1; -.
DR MGSI: MS119+0270; tnfrrsf12.
DR InterPro: IPR000345; Cyt_c_heme_bind.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR SMART: SM00208; TNFR; 3
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ
SEQUENCE 141 AA; 15576 MW; 7552DF3E8PA0EF5F3 CRC64;

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Query Match      21.8, Score 198.5; DB 11; Length 141;
Best local Similarity 32.8%; Pred. No. 2.5e 13;
Matches 41, Conservative 18, Mismatches 59; Indels 7; Gaps

QY 4 CPQKVIHPQNNSTCTCKRIKTYLYNCPQPCQCTPQPSQSSQSSASNNHHPHQLSS 63
   11 1 1 : : 1 1 1 : : : : 1 1 1 : : 1 1 : : 1 1
DB 5 CPAGHY---WKKIWCCNKNNSAGIEVAKKQLETHIQGQCKKCHQKPIPKKINYIADILAS 65
   11 1 1 : : 1 1 1 : : 1 1 : : 1 1 : : 1 1 : : 1 1

QY 64 KCKKIMQIVAFISSIVNHHIVCCQPKQVPHVWSNIPEQENCISQIQCNGTVHLSQPKKQ 122
   11 1 : : 1 1 1 : : 1 1 : : 1 1 : : 1 1 : : 1 1
DB 6H ICEKD--QEMVAIVSATSSKPKKQVPTGIV-VYEPKPEPSPPTKTPQGLVPLVEENSTA 122
   11 1 : : 1 1 1 : : 1 1 : : 1 1 : : 1 1 : : 1 1

QY 121 NTVCT 127
   11111

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ID 123 NTVC5 127
 RESULT 9
 Q9CZA4
 ID Q9CZA4 PRELIMINARY; PRT; 180 AA.
 AC Q9CZA4;
 DT 01-JUN-2001 (TREMBLER). 17, Created)
 DT 01-JUN-2001 (TREMBLER). 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLER). 17, Last annotation update)
 DE 241022806RTR PROTEIN.
 OS TNF5SFAL2 OR 281002806RIK.
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata, Vertebrata, Euteleostomi;
 OC Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SOURCE FROM N.A.
 RC STRAIN=C57H1/6J; TISSUE=EMBRYO;
 RC MCDLINF=21085660; PubMed=11217851;
 RA Kawai J., Shinadawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa T., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kusukawa T., Saito R.,
 RA Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
 RA Koehl P., Lewis S., Matsuo Y., Nishikawa T., Pascale G., Quackenbush J.,
 RA Schriml L.M., Staudli F., Suzuki K., Tomita M., Waquer L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Anno H., Baldarelli P., Barsh G.,
 RA Blake J., Hoffell D., Hojunga N., Catucci P., de Bonaldo M.F.,
 RA Brewster M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hall D., Hofmann C., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Montberis P.,
 RA Norone P., Qing R., Ringwald M., Rodriguez T., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Soya T., Shibata Y., Storch Y.F.,
 RA Suzuki H., Taya Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection."
 FT Nature 409:685-690(2001).
 FL EMBL, AK012838, BAB2852.1, .
 DR MGI:1930270; Trnfrsl2.
 DR InterPro; IPR000345; Cyt_c_heme_bind.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR SMART; SM00208; TNFR; 3.
 DE PROSITE; PS00140, "Y-TCHG-AME", PRKOWN 1.
 DR PROSITE; PS50050, TNFR_NGFR_2, 2.
 SQ SEQUENCE: 180 AA; 20226 MW; F8556E165AD053FA CRC64;

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Query Match      21.1%; Score 198.5; DB 11; Length 180;
Best Local Similarity 32.8%; Pred. No. 9e-13;
Matches 41; Conservative 18, Mismatches 59, Indels 7; Gaps
                                0
QY      4  CQCKYIHHQKNS ICCIKCHKGIYLYNCKGCGQIIDLQCFECSCSFASFNHLKRFCLSLSS 63
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      48  CPAGEY---WSKDVCCNCSAGTFVKAPEIPIITGGCKEKGPGITFEKQNYLLACILIS 104
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      64  KCKKMGQVEIASSCTVIRIIVCGCRKNQYRHYWSNLEQCFNCSICLNG-TVHLSQEQKQ 122
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      105  ICLIKD--QFMVAUCSISDKKCKCKIGLY-YDIPAFPSCKHPCIKCQGIIPVLIQENSLA 161
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      123  NTWCT 127
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      162  NTVC5 166
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
Q9BY86
ID Q9BY86 PPELIMINAPY PPT 417 AA.
AC Q9HY86;
DT 01-JUN-2001 (TRENDSrel. 17, Created)

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DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
 DE 01-JUN-2001 (TREMELrel. 17, Last annotation update)
 DE DEATH RECEPTOR 3.
 GN DR3.
 OS Homo sapiens (Human).
 OC Eukaryota, Metazoa, Chordata, Vertebrata, Euteleostomi,
 OC Mammalia, Eutheria, Primates, Catarrhini, Hominoidea, Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shiozawa S., Konishi Y., Murayama K., Mukae N., Yamamoto K.,
 RA Hayashi S., Sato M., Shiozawa Y., Tsukamoto Y.,
 RT "DR3 genome."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 KW Receptor.
 KW Receptor.
 SQ SEQUENCE 417 AA; 45326 MW; 522631206DB46619 CRC64;

Query Match 21.1%; Score 198.5; DB 4; Length 417;
 Best Local Similarity 29.8%; Pred. No. 6.9e-13;
 Matches 47; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

QY 11 HPONNSICTCKHKGYLYNDGPGQDTDCRETSSTASENHILR-HCLSCSKCRKEM 69
 DB 40 HKKIGLFTGPGPGAPGHVILKAPTEPGNSTVLVQDTFLAWENHINSEAPQACDEQA 99
 QY 70 GVEISSCTVDRITVGGCKNOYRWYSHNLFQC-----FNCISCLN-GTVH-----LSQ 119
 DB 100 SVALENCASAVADTRGCKKPGFVEFC---QVSCVSSSPFYQCLDQCALHPRHILICS 156
 QY 120 EKQNTVCTCHAGFTLPENECVST-----SNCKKSLFQTKLC 155
 DB 157 RRDDGGTCLPGFYEHGDCGVSCPTPPPSL 186

RESULT 11
 ID 014866 PRELIMINARY; PRT: 277 AA.
 AC 014866;
 DT 01-JAN-1998 (TREMELrel. 05, Created)
 DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
 DE SOLUBLE DEATH RECEPTOR 3 BETA
 GN DR3
 OS Homo sapiens (Human).
 OC Eukaryota, Metazoa, Chordata, Vertebrata, Euteleostomi;
 OC Mammalia, Eutheria, Primates, Catarrhini, Hominoidea, Homo
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Warzocha K., Ribeiro P., Charlot C., Goffier R.,
 RA Salles G.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DE EMBL: AF026071; AAB82288.1;
 DE HSSP: P19438; INCP.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 2.
 DR SMART: SM00208; TNFR; 2.
 DR PROSITE: PS001186; EGF_2; UNKNOWN_1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 1.
 SQ SEQUENCE 277 AA; 29111 MW; 3D19F3F847BFC093 CRC64;

Query Match 21.0%; Score 198; DB 4; Length 277;
 Best Local Similarity 31.3%; Pred. No. 4.9e-13;
 Matches 47; Conservative 17; Mismatches 72; Indels 14; Gaps 5;

QY 11 HPONNSICTCKHKGYLYNDGPGQDTDCRETSSTASENHILR-HCLSCSKCRKEM 69
 DB 40 HKKIGLFTGPGPGAPGHVILKAPTEPGNSTVLVQDTFLAWENHINSEAPQACDEQA 99
 QY 70 GVEISSCTVDRITVGGCKNOYRWYSHNLFQC-----FNCISCLN-GTVH-----LSQ 119
 DB 100 SVALENCASAVADTRGCKKPGFVEFC---QVSCVSSSPFYQCLDQCALHPRHILICS 156
 QY 120 EKQNTVCTCHAGFTLPENECVST-----SNCKKSLFQTKLC 155
 DB 157 RRDDGGTCLPGFYEHGDCGVSCPTPPPSL 186

Query Match 21.0%; Score 198; DB 4; Length 277;
 Best Local Similarity 31.3%; Pred. No. 4.9e-13;
 Matches 47; Conservative 17; Mismatches 72; Indels 14; Gaps 5;

QY 11 HPONNSICTCKHKGYLYNDGPGQDTDCRETSSTASENHILR-HCLSCSKCRKEM 69
 DB 40 HKKIGLFTGPGPGAPGHVILKAPTEPGNSTVLVQDTFLAWENHINSEAPQACDEQA 99

QY 70 GVEISSCTVDRITVGGCKNOYRWYSHNLFQC-----FNCISCLN-GTVH-----LSQ 119
 DB 100 SVALENCASAVADTRGCKKPGFVEFC---QVSCVSSSPFYQCLDQCALHPRHILICS 156
 QY 120 EKQNTVCTCHAGFTLPENECVST-----SNCKKSLFQTKLC 149
 DB 157 RRDDGGTCLPGFYEHGDCGVSCPTPPPSL 186

RESULT 12
 ID 014865 PRELIMINARY; PRT: 426 AA.
 AC 014865;
 DT 01-JAN-1998 (TREMELrel. 05, Created)
 DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
 DE DEATH RECEPTOR 3 BETA
 GN DR3.
 OS Homo sapiens (Human).
 OC Eukaryota, Metazoa, Chordata, Vertebrata, Euteleostomi;
 OC Mammalia, Eutheria, Primates, Catarrhini, Hominoidea, Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Warzocha K., Ribeiro P., Charlot C., Goffier R.,
 RA Salles G.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DE EMBL: AF026071; AAB82288.1;
 DE HSSP: P19438; INCP.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 2.
 DR SMART: SM00208; TNFR; 2.
 DR PROSITE: PS001186; EGF_2; UNKNOWN_1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 1.
 SQ SEQUENCE 426 AA; 45950 MW; 371AA7F16A829C16 CRC64;

Query Match 21.0%; Score 198; DB 4; Length 426;
 Best Local Similarity 31.3%; Pred. No. 6.9e-13;
 Matches 47; Conservative 17; Mismatches 72; Indels 14; Gaps 5;

QY 11 HPONNSICTCKHKGYLYNDGPGQDTDCRETSSTASENHILR-HCLSCSKCRKEM 69
 DB 40 HKKIGLFTGPGPGAPGHVILKAPTEPGNSTVLVQDTFLAWENHINSEAPQACDEQA 99
 QY 70 GVEISSCTVDRITVGGCKNOYRWYSHNLFQC-----FNCISCLN-GTVH-----LSQ 119
 DB 100 SVALENCASAVADTRGCKKPGFVEFC---QVSCVSSSPFYQCLDQCALHPRHILICS 156
 QY 120 EKQNTVCTCHAGFTLPENECVST-----SNCKKSLFQTKLC 155
 DB 157 RRDDGGTCLPGFYEHGDCGVSCPTPPPSL 186

RESULT 13
 ID 014865 PRELIMINARY; PRT: 175 AA.
 AC 014865;
 DT 01-MAY-2000 (TREMELrel. 13, Created)
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
 DE DEATH DOMAIN RECEPTOR 3 SOLUBLE FORM (FRAGMENT).
 GN DDR3.

Query Match 21.0%; Score 198; DB 4; Length 426;
 Best Local Similarity 31.3%; Pred. No. 6.9e-13;
 Matches 47; Conservative 17; Mismatches 72; Indels 14; Gaps 5;

QY 11 HPONNSICTCKHKGYLYNDGPGQDTDCRETSSTASENHILR-HCLSCSKCRKEM 69
 DB 40 HKKIGLFTGPGPGAPGHVILKAPTEPGNSTVLVQDTFLAWENHINSEAPQACDEQA 99
 QY 70 GVEISSCTVDRITVGGCKNOYRWYSHNLFQC-----FNCISCLN-GTVH-----LSQ 119
 DB 100 SVALENCASAVADTRGCKKPGFVEFC---QVSCVSSSPFYQCLDQCALHPRHILICS 156
 QY 120 EKQNTVCTCHAGFTLPENECVST-----SNCKKSLFQTKLC 149
 DB 157 RRDDGGTCLPGFYEHGDCGVSCPTPPPSL 186

Query Match 21.0%; Score 198; DB 4; Length 277;
 Best Local Similarity 31.3%; Pred. No. 4.9e-13;
 Matches 47; Conservative 17; Mismatches 72; Indels 14; Gaps 5;

QY 11 HPONNSICTCKHKGYLYNDGPGQDTDCRETSSTASENHILR-HCLSCSKCRKEM 69
 DB 40 HKKIGLFTGPGPGAPGHVILKAPTEPGNSTVLVQDTFLAWENHINSEAPQACDEQA 99

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 111
RP SEQUENCE FROM N.A.
RA Chaudhary P.M., Hood L.E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U83598; AA041433.1; -.
DR HSSP; P19438; 1EXT.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNFR_c6; 2.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 175 AA: 18634 MW: 46468756832157 GPC64;

Query Match 20.8%; Score 196; DB 4; Length 175;
Best Local Similarity 31.5%; Pred. No. 5.4e-13;
Matches 45; Conservative 17; Mismatches 67; Indels 14; Gaps 5;

QY 11 HPONNSIGCTKCHKCTYLYNDPGQDTCRCGCSGTSFTASENHLR-HCLSCSKGRKEM 69
DB 34 HKKIGLFCCKGCPACHYIKAPCTEPGCGNSTCLVPGDTFLAWENHNSKCAKCAQADQA 93
QY 70 GQVEISSCTVDRDTVCGCKKNQYRHYWSENLFQC-----FNCSLCLN-GTVH----LSQ 119
DB 94 SQVALENCSAVADIRGCKRGWVEVC---QVSCQVSSSPFYQCLDQALHRIKLQS 150
QY 120 EKQNTVCTCHAGFFLENFCVSC 142
DB 151 KRDTGCGTCLPGFYRHGDCVSC 173

RESULT 14
Q9UMF0
ID Q9UMF0 PRELIMINARY; PRT; 178 AA.
DI 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE LYMPHOCTE ASSOCIATED RECEPTOR OF DEATH 11 (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 111
RP SEQUENCE FROM N.A.
RA Michael A.J., Bell J.L.;
RL "LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
DR EMBL; U94512; AAC51315.1; -.
DR HSSP; P19438; 1EXT.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNFR_c6; 2.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 178 AA: 19043 MW: 4746868968194 GPC64;

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Query Match 20.8%; Score 196; DB 4; Length 178;
Best Local Similarity 31.5%; Pred. No. 5.5e-13;
Matches 45; Conservative 17; Mismatches 67; Indels 14; Gaps 5;

QY 11 HPONNSIGCTKCHKCTYLYNDPGQDTCRCGCSGTSFTASENHLR-HCLSCSKGRKEM 69
DB 37 HKKIGLFCCKGCPACHYIKAPCTEPGCGNSTCLVPGDTFLAWENHNSKCAKCAQADQA 96
QY 70 GQVEISSCTVDRDTVCGCKKNQYRHYWSENLFQC-----FNCSLCLN-GTVH----LSQ 119
DB 97 SQVALENCSAVADIRGCKRGWVEVC---QVSCQVSSSPFYQCLDQALHRIKLQS 153
QY 120 EKQNTVCTCHAGFFLENFCVSC 142
DB 154 KRDTGCGTCLPGFYRHGDCVSC 176

RESULT 15
Q9UMF1
ID Q9UMF1 PRELIMINARY; PRT; 181 AA.
DI 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE LYMPHOCTE ASSOCIATED RECEPTOR OF DEATH 4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 111
RP SEQUENCE FROM N.A.
RA Michael A.J., Xu X.N., Olsen A.L., Cowper A.F., Tan R.;
RL "LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
DR EMBL; U94505; AAC51310.1; -.
DR HSSP; P19438; 1EXT.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNFR_c6; 2.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 181 AA: 13432 MW: 59AAFE56646569 GPC64;

Query Match 20.8%; Score 196; DB 4; Length 181;
Best Local Similarity 31.5%; Pred. No. 5.5e-13;
Matches 45; Conservative 17; Mismatches 67; Indels 14; Gaps 5;

QY 11 HPONNSIGCTKCHKCTYLYNDPGQDTCRCGCSGTSFTASENHLR-HCLSCSKGRKEM 69
DB 40 HKKIGLFCCKGCPACHYIKAPCTEPGCGNSTCLVPGDTFLAWENHNSKCAKCAQADQA 99
QY 70 GQVEISSCTVDRDTVCGCKKNQYRHYWSENLFQC-----FNCSLCLN-GTVH----LSQ 119
DB 106 SQVALENCSAVADIRGCKRGWVEVC---QVSCQVSSSPFYQCLDQALHRIKLQS 156
QY 120 EKQNTVCTCHAGFFLENFCVSC 142
DB 157 KRDTGCGTCLPGFYRHGDCVSC 179

Search completed: April 24, 2002, 10:46:49
Job time: 617 sec

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